



Docket No.: CL001013CIP
Serial No.: 09/829,432
Inventors: KETCHUM, Karen A. et al.
Title: ISOLATED HUMAN TRANSPORTER...

APPROVED BY DRAFTSMAN	O.G. FIG.	SUBCLASS
	CLASS	

1 GCCCTTGGCA GCAGCCCTGT TACCGCTTAG ATGGCGCGCA GGACAGAGCC
51 CCCCACGCGG GGCTGGGGAC GGGTGGTGGT GCTCTCAGCG TTCTTCCAGT
101 CGGCGCTTGT GTTTGGGGTG CTCCGCTCCT TTGGGGTCTT CTCGTGGAG
151 TTTGTGGCGG CGTTTGAGGA GCAGGCAGCG CGCGTCTCCT GGATCGCCTC
201 CATAGGAATC GCGGTGCAGC AGTTTGGGAG CCCGGTAGGC AGTGCCCTGA
251 GCACGAAGTT CGGGCCAGG CCCGTGGTGA TGA CTGGAGG CATCTTGGCT
301 GCGCTGGGGA TGCTGCTCGC CTCTTTTGCT ACTTCCTTGA CCCACCTATA
351 CCTGAGTATT GGGTTGCTGT CAGGCTCTGG CTGGGCTTTG ACCTTCGCTC
401 CGACCCTGGC CTGCCTGTCC TGTATTCT CTGCGCAGC ATCCCTGGCC
451 ACCGGGCTGG CACTGACAGG CGTGGGCCTC TCCTCCTTCA CATTGCCCC
501 CTTTTTCCAG TGGCTGCTCA GCCACTACGC CTGGAGGGGG TCCCTGCTGC
551 TGGTGTCTGC TCTCTCCCTC CACCTAGTGG CCTGTGGTGC TCTCCTCCGC
601 CCACCCTCCC TGGCTGAGGA CCCTGCTGTG GGTGGTCCCA GGGCCCAACT
651 CACCTCTCTC CTCCATCATG GCCCCTTCCT CCGTTAACT GTTGCCCTCA
701 CCTTGATCAA CACTGGCTAC TTCATTCCCT ACCTCCACCT GGTGGCCCAT
751 CTCCAGGACC TGGATTGGGA CCCACTACCT GCCGCCTTCC TACTCTCAGT
801 TGTGCTATT TCTGACCTCG TGGGGCGTGT GGTCTCCGGA TGGCTGGGAG
851 ATGCAGTCCC AGGGCCTGTG ACACGACTCC TGATGCTCTG GACCACCTTG
901 ACTGGGGTGT CACTAGCCCT GTTCCCTGTA GCTCAGGCTC CCACAGCCCT
951 GGTGGCTCTG GCTGTGGCCT ACGGCTTCAC ATCAGGGGCT CTGGCCCCAC
1001 TGGCCTTCTC TGTGCTGCCT GAACTAATAG GGA CTAGAAG GATTTACTGT
1051 GGCTGGGAC TGTGCAGAT GATAGAGAGC ATCGGGGGGC TGCTGGGGCC
1101 TCCTCTCTCA GGCTACCTCC GGGATGTGTC AGGCAACTAC ACGGCTTCTT
1151 TTGTGGTGGC TGGGGCCTTC CTCTTTTCAG GGAGTGGCAT TCTCCTCACC
1201 CTGCCCCACT TCTTCTGCTT CTCAACTACT ACCTCCGGGC CTCAGGACCT
1251 TGTAACAGAA GCACTAGATA CTAAAGTTCC CCTACCCAAG GAGGGGCTGG
1301 AAGGAGGACT GAACTCCACA GAGTCAGGCC CAGAAAGCCA AAGCTTGACA
1351 GCTCCAGGTC TTCTCTTGCC ACGTCTTGGT CTCCACAGAA CCACAGTGCC
1401 TTAAGATTCT TGATCTGCCT CCCCTAGAG CAGGCCTGGG GCTCCTGCAA
1451 TGTGTGTGCC AACCTTTT (SEQ ID NO:1)

FEATURES:

5'UTR: 1-30
Start Codon: 31
Stop Codon: 1402
3'UTR: 1405

FIGURE 1A



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HOMOLOGOUS PROTEINS:

Top 10 BLAST Hits:

		Score	E
CRA	103000001515981 /altid=gi 7670446 /def=dbj BAA95074.1 (AB0...	250	3e-65
CRA	150000165029756 /altid=gi 13431667 /def=sp O70461 MOT3_RAT ...	244	1e-63
CRA	89000000192725 /altid=gi 10048452 /def=ref NP_065262.1 sol...	238	8e-62
CRA	18000005042369 /altid=gi 2497855 /def=sp Q63344 MOT2_RAT MO...	238	1e-61
CRA	18000005039313 /altid=gi 1432167 /def=gb AAB04023.1 (U6231...	238	1e-61
CRA	18000005141743 /altid=gi 6755536 /def=ref NP_035521.1 solu...	234	2e-60
CRA	335001098681302 /altid=gi 11418102 /def=ref XP_009979.1 mo...	234	2e-60
CRA	1000682335761 /altid=gi 7019529 /def=ref NP_037488.1 monoc...	233	5e-60
CRA	18000005141744 /altid=gi 4759120 /def=ref NP_004722.1 solu...	232	6e-60
CRA	108000024650708 /altid=gi 12737028 /def=ref XP_012127.1 so...	232	6e-60

BLAST dbEST hits:

	Score	E
gi 8423571 /dataset=dbest /taxon=960...	733	0.0

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

From BLAST dbEST hits:

gi|8423571 breast

From tissue screening panels:

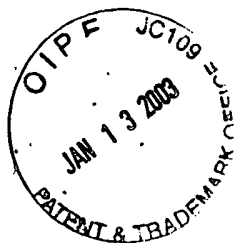
Spleen

Breast (adult)

APPROVED BY DRAFTSMAN	O.G. FIG.
	CLASS SUBCLASS

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TECH CENTER 1600/2900

FIGURE 1B



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APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

1 MARRTEPPDG GWGRVVVLSA FFQSALVFGV LRSFGVFFVE FVAAFEEQAA
51 RVSWIASIGI AVQQFGSPVG SALSTKFGPR PVVMTGGILA ALGMLLASFA
101 TSLTHLYLSI GLLSGSGWAL TFAPTLACLS CYFSRRRSLA TGLALTGVGL
151 SSFTFAPFFQ WLLSHYAWRG SLLLVSA LSL HLVACGALLR PPSLAEDPAV
201 GGPRAQLTSL LHHGPFLRYT VALTLINTGY FIPYLHLVAH LQDLWDWPLP
251 AAFLLSVVAI SDLVGRVVSG WLGDVPGPV TRLLMLWTTL TGVSLALFPV
301 AQAPTALVAL AVAYGFTSGA LAPLAFSVLP ELIGTRRIYC GLGLLQMIES
351 IGGLLGPPLS GYL RDVSGNY TASFVVAGAF LLSGSGILLT LPHFFCFSTT
401 TSGPQDLVTE ALDTKVPLPK EGLEGGLNST ESGPESQSLT APGLLLPRLG
451 LHRTTVP (SEQ ID NO:2)

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

Number of matches: 2

- 1 369-372 NYTA
- 2 428-431 NSTE

[2] PDOC00004 PS00004 CAMP_PHOSPHO_SITE
cAMP- and cGMP-dependent protein kinase phosphorylation site

135-138 RRRS

[3] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 3

- 1 74-76 STK
- 2 134-136 SRR
- 3 335-337 TRR

[4] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 2

- 1 193-196 SLAE
- 2 432-435 SGPE

[5] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 18

- 1 29-34 GVLRSF
- 2 66-71 GSPVGS
- 3 70-75 GSALST
- 4 86-91 GGILAA
- 5 87-92 GILAAL
- 6 93-98 GMLLAS
- 7 111-116 GLLSGS
- 8 115-120 GSGWAL
- 9 142-147 GLALTG
- 10 147-152 GVGLSS
- 11 201-206 GGPRAQ
- 12 292-297 GVSLAL
- 13 368-373 GNYTAS
- 14 386-391 GILLTL
- 15 422-427 GLEGGL

FIGURE 2A



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BLAST Alignment to Top Hit:

>CRA|150000165029756 /altid=gi|13431667 /def=sp|070461|MOT3_RAT
MONOCARBOXYLATE TRANSPORTER 3 (MCT 3) /org=MCT 3
/dataset=nraa /length=492
Length = 492

Score = 244 bits (617), Expect = 1e-63
Identities = 168/470 (35%), Positives = 239/470 (50%), Gaps = 36/470 (7%)

Query: 3 RRTEPPDGGWGRVVLSAFFQSALVFGVLRSGVFFVEFVAAFEEQAARVSWIASIGIAV 62
R PPDGGWG VV+ + F + +G ++ VFF E F + +W++SI +A+
Sbjct: 8 RGAGPPDGGWGWWVLGACFVITGFAYGFPKAVSVFFRELKRDFGAGYSDTAWVSSIMLAM 67

Query: 63 QQFGSPVGSALSTKFGPRPVMTGGILAAALGMLLASFATSLTHLYLSIGLLSGSGWALTF 122
P+ S L T+FG RPV++ GG+LA+ GM+LASFA+ L LYL+ G+L+G G AL F
Sbjct: 68 LYGTGPLSSILVTRFGCRPVMLAGLLASAGMILASFASRLLELYLTAGVLTGLGLALNF 127

Query: 123 APTLACLSCYFSRRRSLATGLALTGVGLSSFTFAPFFQWLLSHYAWRGSLLLVSALSILHL 182
P+L L YF RRR LA GLA G + T+P Q L + WRG LL L LH
Sbjct: 128 QPSLIMLGlyFERRRPLANGLAAAGSPVFLSTLSPLGQLGERFGWRGGFLLFGGLLLHC 187

Query: 183 VACGALLRPPSLAE---DPAVGGPRAQLTSLH-----HGPFLRYTVALTLINTGYFIPY 234
ACGA++RPP + DPA G RA+ LL F+ Y V L+ G F+P
Sbjct: 188 CACGAVMRPPPGPQPRDPAPPGGRARHRQLLDLAVCTDRTFMVVMVTKFLMALGLFVPA 247

Query: 235 LHLVAHLQDLWDPLPAAFLLSVVAISDLVGRVSWGVLG--DAVPGPVTRLMLWTTLTG 292
+ LV + +D AAFLLS+V D+V R G L + V L L G
Sbjct: 248 ILLVNYAKDAGVPDAEAAFLLSIVGFVDIVARPACGALAGLRLRPHVPYLFSLALLANG 307

Query: 293 VSLALFPVAQAPTALVALAVAYGFTSGALAPLAFSVLPELIGTRRIYCGLLQMIESIG 352
++ + A++ LVA +A+G + G + L F VL +G R LGL+ ++E++
Sbjct: 308 LTDLISARARSYGTLVAFCIAFGLSYGMVGALQFEVLMATVGAPRFPSPALGLVLLVEAVA 367

Query: 353 GLLGPPLSGYL RDVSGNYTASFVVAGAFLLSGSGILLTLPHFFCFSTT----- 400
L+GPP +G L D NY F +AG+ ++ +G+ ++ + C +
Sbjct: 368 VLIGPPSAGRLVDALKNYEIIIFYLAGS-EVALAGVFMAVTTYCCLRCSKNISSGRSAEGG 426

Query: 401 TSGPQDLVTEALDTKVPLPKEGLEGGLNSTESGPESQSLTAPGLLLPRLG 450
S P+D+ EA P+P STE E SL A +L PR G
Sbjct: 427 ASDPEDV--EAERDSEMPA-----STE---EPGSLEALEVLSPRAG 463 (SEQ ID
NO:4)

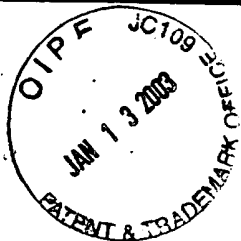
>CRA|89000000192725 /altid=gi|10048452 /def=ref|NP_065262.1| solute
carrier family 16 (monocarboxylic acid transporters),
member 8; proton-coupled monocarboxylate transporter 3
gene; proton-coupled monocarboxylate transporter 3 [Mus
musculus] /org=Mus musculus /taxon=10090 /dataset=nraa
/length=492
Length = 492

Score = 238 bits (602), Expect = 8e-62
Identities = 165/470 (35%), Positives = 236/470 (50%), Gaps = 36/470 (7%)

Query: 3 RRTEPPDGGWGRVVLSAFFQSALVFGVLRSGVFFVEFVAAFEEQAARVSWIASIGIAV 62
R PPDGGWG VV+ + F + +G ++ VFF E F + +W++SI +A+
Sbjct: 8 RGAGPPDGGWGWWVLGACFVVTGFAYGFPKAVSVFFRELKRDFGAGYSDTAWVSSIMLAM 67

Query: 63 QQFGSPVGSALSTKFGPRPVMTGGILAAALGMLLASFATSLTHLYLSIGLLSGSGWALTF 122
P+ S L T+FG RPV++ GG+LA+ GM+LASFA+ L LYL+ G+L+G G AL F

FIGURE 2C

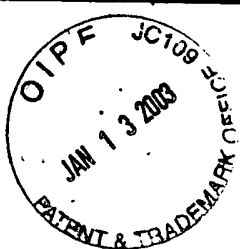


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Sbjct: 68 LYGTGPLSSILVTRFGCRPVMLAGLLASAGMILASFASRLVELYLTAGVLTGLGLALNF 127

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
CRAFTSMAN		

FIGURE 2D



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Query: 123 APTLACLSCYFSRRRSLATGLALTGVGLSSFTFAPFFQWLLSHYAWRGSLLLVSALS LHL 182
P+L L YF RRR LA GLA G + +P Q L + WRG LL L LH
Sbjct: 128 QPSLIMLGlyFERRRPLANGLAAAGSPVFLSMLSPLGQLLGERFGWRGGFLLFGGLLLHC 187

Query: 183 VACGALLRP---PSLAEDPAVGGPRAQLTSLH-----HGPFLRYTVALTLINTGYFIPY 234
ACGA++RP P DP+ G A+ LL F+ Y V L+ G F+P
Sbjct: 188 CACGAVMRPPPGPPRRDPSPHGGPARRRRLLDVAVCTDRAFVVVVTKFLMALGLFVPA 247

Query: 235 LHLVAHLQDLWDPLPA AFLLSVVAISDLVGRVVSGLG--DAVPGPVTRLMLWTTTLTG 292
+ LV + +D AAFLLS+V D+V R G L + V L L G
Sbjct: 248 ILLVNYAKDAGVPDAEA AFLLSIVGFVDIVARPACGALAGLGRLRPHVPYLFSLALLANG 307

Query: 293 VSLALFPVAQAPTALVALAVAYGFTSGALAPLAFSVLP ELIGTRRIYCGLLQMIESIG 352
++ + A++ LVA +A+G + G + L F VL +G R LGL+ ++E++
Sbjct: 308 LTDLISARARSYGTLVAFCI AFGLSYGMVGALQFEVLMATVGAPRFPSALGLVLLVEAVA 367

Query: 353 GLLGPPLSGYLRDVSNGNYTASFVAVAGAFLLSGS GILLTLPHFFCFSTT----- 400
L+GPP +G L D NY F +AG+ ++ +G+ + + C +
Sbjct: 368 VLIGPPSAGRLVDALKNYEII FYLAGS-EVALAGVFMAVTTYCCLRCSKNISSGRSAEGG 426

Query: 401 TSGPQDLVTEALDTKVPLPKEGLEGGLNSTESGPESQSLTAPGLLLPRLG 450
S P+D+ EA P+P STE E SL A +L PR G
Sbjct: 427 ASDPEDV--EAERDSEMPA-----STE---EPGSLEALEVLSPRAG 463 (SEQ ID
NO:5)

Hammer search results (Pfam):

Model	Description	Score	E-value	N
PF01587	Monocarboxylate transporter	204.9	1.2e-57	2
PF01925	Domain of unknown function	4.4	4.6	1
PF00348	Polyprenyl synthetases	3.7	6.1	1
PF00083	Sugar (and other) transporter	3.0	3.8	1
PF01306	LacY proton/sugar symporter	2.7	6.6	1
PF01309	Equine arteritis virus small envelope glycop	2.3	5	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF01925	1/1	65	97 ..	165	201 .]	4.4	4.6
PF00083	1/1	12	108 ..	1	113 [.	3.0	3.8
PF01309	1/1	153	173 ..	1	21 [.	2.3	5
PF00348	1/1	174	191 ..	1	19 [.	3.7	6.1
PF01587	1/2	20	192 ..	1	191 [.	160.8	2.3e-44
PF01587	2/2	219	377 ..	441	611 .]	48.3	1.6e-12
PF01306	1/1	373	393 ..	393	415 .]	2.7	6.6

FIGURE 2E



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APPROVED	O.G. FIG.	
	CLASS	SUBCLASS
BY	DRAFTSMAN	

1 CATT TTTTAGT GCATGGATT TCTAACTGAA CCCCTTGGGC AACGCTTAAT
51 AGTAGGTA CT ATTATCCCCA GTTACAGAT GGGGAAACCA ACTGAGAGAT
101 TCAGCATCTT GATCGAGTTA AGTAATAAAG TCAAGATTGG AACTGGGCCA
151 GGCACGGTGG CTCACGCCTG TAATCCCAGC ACTTTGGGAG GCCAAGGCTG
201 GTGGATCACT TGAGGTGAGG AGTTCGAGAC CAGCGTGGCC AACATGGTGA
251 GACCTCGTCT CTACTAAAAA TACCAAAATT AACTGGGCGT TGTGGTGGGA
301 GCCTGTAATC CCAGAAACTC AGGAGACTGA GGCAGGAGAA TCACTTGAAC
351 CCGGGAGGTG GAGGTGCGAG TGAGCCAAGA TCATGCCACT GCACTCCAGC
401 CTGGGCCACA GAGCAAGACT CCGTCTCAAA ATAAATAAAT AAATAAATAA
451 ATAAATAAAA GACTGGAAC TGTATCTGAT TCTAAAGACC CGAGTCTTCTA
501 ATCACTATGT AATACAGCCA CAGCAATTTT TGTATCTTTG GCATATTCCC
551 CACCAGCCGA CATTTTGACT CTTAGAAAGT ATATATGTGT ATTATTGATG
601 ATTACTTTTA TTTCCCATAT ATAAAATTAT TTAAGGCTCA ATATGTCTTT
651 TAAGACTGCA CACCTCCCTC CCTGCCTCCA CTTCTTGT TT GCTGCTTTCC
701 CCAGTAATCT GGGAGTGAAC ATTGAGTCCA CGGTTTCAAG GTCAGGGTCC
751 TGGGAAGTAT GGCTTATAAT GAAGGAACAG GAAATCCAAG CCATTGGTGT
801 TATGGAGACT GGAAGGACT GGGGAGTGT TGTAGGGGC CTGAGGACTA
851 CTTGGGTAAAG AGGGGCTGA CTGCTCCAGT GGCCAGGGTC ATAGTTTTGT
901 CTCTTTAGTC TACCCACCA TCAGATCAAA AAAGGTGGT AGGAAGTGGT
951 TGTACTAGA GGCAGAGGA AAAGGTTCCTA GCCCAGTGA GGAAGAGGTA
1001 GGTGTGTGTG GTGGGCCCT GTGTGAGCTT ACAGCCGCC TTCTCTCTCT
1051 CAGTTATTTT TGTCTCTGT GACCTGTAGG TTTCTGTTA GTGGGAACAG
1101 AAGTGACAGG AACGAGTTCC CACTACAGAA ATGAACGCCA GGAGTCCAAC
1151 TCATTCCCTT TCTCTCTTCC CTTAGCCGTT GAACTTCTCA GGGATCCAGG
1201 CTTCTAGGTC TCGTGCCTA GGGCTGCGTG TTAGTGGCTT CAGGCGCTGC
1251 GCCAAACACT TCGTTTGAGT CTCATCTCTT AACCCCTCCC CTACCCCAA
1301 CAGGGCCTTG CAATTCCTGG ACCCTCATT AAAGCAAGAG AGTCTCTCTC
1351 TCTCCAGACC CAGTTTACCC ACCACTAACC CTTCCGTGTG GCTCTGGGTG
1401 CTGAAACGGG GATGACTTGG CCCGCTAGGT GAAGAGGAGA CGGAAGCTTC
1451 CTGGCAGTCC CCGCGTCACG TGGGGCCCTA CCTAGTCAGC CTCCTAACGC
1501 CCTCCTTAC GCATGCGCCC ATTCAGTCTT GGTCCCAAC AATGCCTAAA
1551 TCCCGCCCTG CCCTTCTCGT TCCGCCCTG CCGGGAGCC CCGCGTCTC
1601 ATTGGCGAGC TCCAGGGTGG CCCGGCCCGG ACACCCAGT GATAAAATAG
1651 ATCACTTACA CGGAAACTGG CGCGCTCCAG GGTGGGGCC CAACTCAGT
1701 TCCACCCTCT GGCTCCAGC CGAACACCGA ACCGGGACCG ATCCGGCCCC
1751 GGCTTGAAC AGCTCAGCTC CGAGCTCGCG GAACCACGCC CCCGGGAGAC
1801 TCTGGCCCGG CCAGCGCGGG CCAGGTCTTC AGTCTATAT CGCCCTGCCT
1851 TGGGAAAAGG TGCAGGGGCC TCTCGCCGCC TCGTGGGGC CTTCTCTCT
1901 ACCTGCCTCT CCAACCCCTC TCGGCCCGA GCCACCCGGC AGCGGGGGTG
1951 GGTGTGCAGA GGTGCGGCT CCAGAACCCG GCTCCTGCAG AGGCTCTGGG
2001 TGGCAGCAGC CCTGTTACCG CTTAGATGGC GCGCAGGACA GAGCCCCCG
2051 ACGGGGGCTG GGGATGGGTG GTGGTGTCT CAGCGTTCTT CCAGTCGGCG
2101 CTTGTGTTTG GGGTGTCTCG CTCCTTGGG GTCTTCTTCG TGGAGTTTGT
2151 GCGGCGT TTT GAGGAGCAGG CAGCGCGCT CTCCTGGATC GCCTCCATAG
2201 GAATCGCGGT GCAGCAGTTT GGGAGTGAGT GCGGCGCTG GATCTGGCGG
2251 ACTGCGACCC TCGGAAGGGA GAGGGAATGC GCGACTGGG AAGTGAAGG
2301 GCGAGGGGCG GGAGATGCTG GGGGGGAGAC CCCTGAGATC TTCTCGCAGC
2351 GCCCCTTCCA CTTCTCAGG CCCGGTAGGC AGTGCCCTGA GCACGAAGTT
2401 CCGGCCAGG CCCGTGTGTA TGA CTGAGG CATCTTGGCT GCGCTGGGGA
2451 TGCTGCTCGC CTCTTTTGT ACTTCTTGA CCCACCTATA CTTGAGTATT
2501 GGGTTGCTGT CAGGTGAGAG CTTGCACAAG GGCAGGAGAG TCAAATGCTT
2551 AGATCGTTTG ATGTTACCT CTTCTCTGCT CTTTCAAAG GGTTCGGGGA
2601 GAAGCTGAGG GAAAGTTTAG CTAGCACCTG TACCAGAAG GGAATTCTTA
2651 ATAGGAATGA CTAAAGCGAC AAACATGGTG AGGAATTAGG AAATTCAAGG
2701 ATGATGAAAC CTGGCCAGGC ACGGTGGCTC ACGCTGTAA TCCCAGCACT
2751 TTGGGAAGCC GAGGCGGGTG GATCAGAGG TCAGGAGTTT GAGACCAGCC
2801 TGGCCAACAT GGTGAAACCC CGTCTCTACA AAAATACAAA AATTAGCCCG
2851 GCCTGGTGGC GCTAATCCCA GTTACTCGGG AGGCTGAGGC AGGAGAATCG
2901 CTTGAACCCG GAGGCGGAG GTTGCAGTGA GCCAAGATCG CACCACTGCA
2951 CTCCAGCCTG GCGCAGAG CAAGATTCTG TCTCAAAAAA AAAAAAAAAA

FIGURE 3A

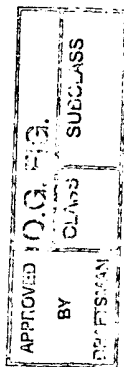


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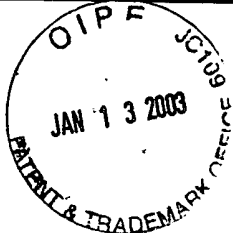
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3001 AAAAAAAAAA AGATGAAACC AAGTATACAA GCCCAGAAGC CTAGGGCTAA
3051 TGGGACTGGA GTGCAAAAGG AAGAATTACT ATAAAAATGGT GCTAGGGGCC
3101 AGGCACGGTG GCTCACGCCT GTAATCCCAG CACTTTGGGA GGCCGAGGCG
3151 GCGGATCAC GAGGTCAGGA GATCAAGACC ATCCTGGCTA ACACGGTGAA
3201 ATCACGTCTC TACTAAAAAC ACAAAAAATT AGCTGGGCGT GGTGGCAGGT
3251 GACTGTAGTC CCAGCTACTC GGGAGGCTGA GGCAGGAGAA TGGTGTGAAC
3301 CCGGGAAGCA GAGCTTGCAG TGAGCCGAGA TTGCACCCT GCACTCCAGC
3351 CTGGGGGACA GAGCGAGACT CCGTCTCAAA AAAAAAAGA AAAAAAAGG
3401 TGCTAGGTAC TGTGACTGTG AAATCGATAT CATTATTGGA TTTACAGCTG
3451 GGGAAAAGCT TTAAAGCTTA TACAACCTGG CAAATGAAGG TCACACAGCT
3501 AGAAATGGTA GAGCCAGGT CTAACCTCAA AGTTCTGTGC TAGTTACCTT
3551 ACAAACCTTG TCTCTAATCT TCCACAATCC CAAAAAGTGT ATTATTACAT
3601 TTTGCAGTTG AGAAGGTTGA GGCTGGGGGT GTTAAGTAAA ACACACAAGG
3651 TTACACAGCT ATGAAGTATC CAAGCCAAGA TTGTATCCCA GGTCTGTGGG
3701 ACTCCGAAGC AAGTGCTACA TTCTGCTGCT GGGCAATGCG GGGATTACTG
3751 TGTGCCTTGA GCTCCCTAAG AGTTCTCAAC ACCACTTCTT CCTTTTGTAC
3801 AGGCTCTGGC TGGGCTTTGA CCTTCGCTCC GACCCTGGCC TGCCTGTCTT
3851 GTTATTTCTC TCGCCGACGA TCCTGGCCA CCGGGCTGGC ACTGACAGGC
3901 GTGGGCTCTT CCTCCTTCAC ATTTGCCCCC TTTTTCAGT GGCTGCTCAG
3951 CCACTACGCC TGGAGGGGGT CCCTGCTGCT GGTGCTGTCC CTCTCCCTCC
4001 ACCTAGTGGC CTGTGGTGCT CTCCTCCGCC CACCCTCCCT GGCTGAGGAC
4051 CCTGCTGTGG GTGGTCCCAG GGCCCAACTC ACCTCTCTCC TCCATCATGG
4101 CCCCTTCCTC CGTTACACTG TTGCCCTCAC CCTGATCAAC ACTGGCTACT
4151 TCATTCCCTA CCTCCACCTG GTGGCCCATC TCCAGGACCT GGATTGGGAC
4201 CCACTACCTG CTGCCCTTCT ACTCTCAGT GTTGCTATTT CTGACCTCGT
4251 GGGGCGTGTG GTCTCCGGAT GGCTGGGAGA TGCAGTCCCA GGGCCTGTGA
4301 CACGACTCCT GATGCTCTGG ACCACCTTGA CTGGGGTGTC ACTAGCCCTG
4351 TTCCCTGTAG CTCAGGCTCC CACAGCCCTG GTGGCTCTGG CTGTGGCCTA
4401 CGGCTTCACA TCAGGGGGCTC TGGCCCCACT GGCCTTCTCT GTGCTGCCCTG
4451 AACTAATAGG GACTAGAAGG ATTTACTGTG GCCTGGGACT GTTGACAGATG
4501 ATAGAGAGCA TCGGGGGGCT GCTGGGGCCT CCTCTCTCAG GTAAGTGGAA
4551 TGGGGTTCCC AGGGGGTGAG GGCTGCCATG TTGCACAACT AGGGGAGGGT
4601 ACTATTCTCA TTACAGTGTA TGTGAATATT GCCCTCTGGT GTAGTACAGT
4651 ACACAGCCTG CTGGGCCAAC CATAGCATCC CTGAAATGGG TCCATGGGGC
4701 AAAGAAGCTT GGGCTGGGAA AGTCTGAGTG GAAAGACAAA AAGAAGCTAA
4751 GTGGAACCTT TGGCAGGGTG CCTACGGCTT GGGTTTGCAG AGGACCTGGC
4801 AGAACCTGGC CAGACACAGA CGTAGCATTC CAGTGTGCAC CCTTTCCTTT
4851 GGCCTACTGG GCCCCAAACC AGGTATCTGA GGCACCTGGT CAAAGTTCTG
4901 CTGGCTCAGG GTGCCAGAAC TTTCAGACCT TTATCTCCTC TTACCCATTA
4951 ACTGAAGCTT TAGAAAAGCC ACAGTTGGTG GCGCCTGTA GTCCAGCTA
5001 CTCAGGAGGC TGAGGCAGGA GAATGGCATG AACCCGGGAG GCGGAGCTTG
5051 CAGTGAGCTG AGATCGCGCC ACTGCACTTC AGCCTGGGCG ACAGAGCGAG
5101 ACTCCGTCTC AAAAAAAAAA AAAAAAGAAA GGCCACAGTT GCCAGAAAGA
5151 AAGGCACAAG TATGCCTGAC TCAATCTGGA TCTCCAAATC CCTGCAGGCT
5201 GGTTTGGAGG TCCTTTCTGA AGGCGGGGAG GTGGTTGAAA TTAACCTTTG
5251 AGGCCCTTTT GGGAAACGAG AGTTCTTAAG TTTATCCAAC TATTCCATGG
5301 GAGTTCCAAC TCCTCTGAGA TGATAAGTCT TCCCTCCACC CAAAAATGTA
5351 TCTGAGCCCT CAGCCCCAGC AAATAGATCA CTCATGTGTA TTCTTTTCTT
5401 CTCTTGGAAC TAGGCTACCT CCGGATGTG ACAGGCAACT ACACGGCTTC
5451 TTTTGTGGTG GCTGGGGCCT TCCTTCTTTC AGGGAGTGGC ATTCTCCTCA
5501 CCCTGCCCCA CTCTTCTGCT TTCTCAACTA CTACCTCCGG GCCCAGGAC
5551 CTTGTAACAG AAGCACTAGA TACTAAAGTT CCCCTACCCA AGGAGGGACT
5601 GGAAGGAGGA CTGAACCTCCA CAGAGTCAGG CCCAGAAAGC CAAAGCTTGA
5651 CAGCTCCAGG TCTTCTCTTG CCACGTCTTG GTCTCCACAG AACCACAGTG
5701 CCTTAAGATT CTTGATCTGC CTCCCCCTAG AGCAGGCCTG GGGCTCCTGC
5751 AATGTGTGTG CCAACCCCTT GTATTTTGTG GAGGACTCTT ATTTCTCCGT
5801 TACTCTCCTA ACCTTTTCTT CTTTTTCTT TTTCCCGAGA CGGAGTCTTG
5851 CTCTGTGGC CAGGCTGGAG TGCAGTGATG TGATCTCGGC TCACTGCAAC
5901 CTCCGCTTCC CGGTTTCAAG CGATTCTCCT GCCTCAGCCT CCCAAGTAGC
5951 TGGGATTACA GGCGGGAGCC ACCACACCCG GCTATTTTTT TTTTTTTTTT

FIGURE 3B



Docket No.: CL001013CIP
Serial No.: 09/829,432
Inventors: KETCHUM, Karen A. et al.
Title: ISOLATED HUMAN TRANSPORTER...

6001 TTTNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNTTTTGG TAGAGACAGG
6051 GTTTCACCAT GTTGCCAGG ATGGTCTCGA ACTCCTGACC TTGTGATCCA
6101 CCCCCCGCCC CTCCCTCGGC CTTCCAAAGT GCTGGGATTA CAGGCGTGAG
6151 CCACCACACC CAGCCTCCCC TAACCTTTTC TAAAGGACCC AGGAGTTTGG
6201 AAGGATCCGG GAGTTCCTGC TTCACTGAGC TGTGAATCAA CTGTGAAAAT
6251 CAAAGGCCAA GAGACTTATC ATGCTTTATA TAACATCTCT AGTGTTCGCT
6301 CCTGAGTTTC TTCTCTGAAG ACACATGTTT GGGAAACAAA ACTGTCCCTT
6351 TGAGATAAAA TCAAATAAGA AAATTGGATA ATAATCACAA CCTCAAAATG
6401 AGCTGGGGCC CATATGCTTG GGTGGCCGA ATGGAGTCAT GCCTGGAAGT
6451 GGAGGAGAGT GTCCAGGAGC TCCGATGACC CAAGGCATT TAACCCTGGA
6501 ATCTGCTCTC CAGGCTACCA CCACATACCT CCCTCTTCCC CATTATCCCT
6551 GTGGCTTAGA AAAGAA (SEQ ID NO:3)

FEATURES:

Start: 2026
Exon: 2026-2224
Intron: 2225-2369
Exon: 2370-2513
Intron: 2514-3802
Exon: 3803-4540
Intron: 4541-5413
Exon: 5414-5703
Stop: 5704

CHROMOSOME MAP POSITION:

Chromosome 17

ALLELIC VARIANTS (SNPs):

DNA				Protein		
Position	Major	Minor	Domain	Position	Major	Minor
423	G	A	Beyond ORF (5')			
2717	A	G	Intron			
3064	C	T	Intron			
4146	C	A	Exon	229	G	G
4440	T	C	Exon	327	S	S
4443	G	T	Exon	328	V	V
5105	T	C	Intron			

Context:

DNA

Position

423 TAATAAAGTCAAGATTGGAAGTGGGCCAGGCACGGTGGCTCACGCCTGTAATCCCAGCAC
TTTGGGAGGCCAAGGCTGGTGATCACTTGAGGTCAGGAGTTCGAGACCAGCGTGGCCAA
CATGGTGAGACCTCGTCTCTACTAAAAATACCAAAATTAAGTGGGCGTTGTGGTGGGAGC
CTGTAATCCCAGAACTCAGGAGACTGAGGCAGGAGAATCACTTGAACCCGGGAGGTGGA
GGTTGCAGTGAGCCAAGATCATGCCACTGCACTCCAGCCTGGGCCACAGAGCAAGACTCC
[G,A]
TCTCAAAATAAATAAATAAATAAATAAATAAATAAAGACTGGAAGTGTGATCTGATTCT
AAAGACCCGAGTTCTTAATCACTATGTAATACAGCCACAGCAATTTCTGTATCTTTGGCA
TATTCCCCACCCAGCCGACATTTGACTCTTAGAAAAGTATATATGTGTATTATTGATGATT
ACTTTTATTTCCACATATAAAATTATTTAAGGCTCAATATGTCTTTTAAGACTGCACAC
CTCCCTCCCTGCTCCACTTCTGTTTGCTGCTTTCCCCAGTAATCTGGGAGTGAACATT

2717 GTGATGACTGGAGGCATCTTGGCTGCGCTGGGGATGCTGCTCGCCTCTTTGCTACTTCC
TTGACCCACCTATACCTGAGTATTGGGTTGCTGTCAGGTGAGAGCCTGCACAAGGGCAGG
AGAGTCAAATGCTTAGATCCTTGGATGTTACCTCCTTCTGCTCCTTCCAAAGGGTTCG
GGGAGAAGCTGAGGGAAAGTTAGCTAGCACCTGTACCCAGAAGGGAATTCTTAATAGGA

FIGURE 3C

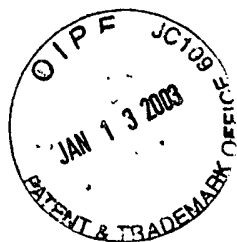


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ATGACTAAAGCGACAAACATGGTGAGGAATTAGGAAATTCAAGGATGATGAAACCTGGCC
[A, G]
GGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAAGCCGAGGCGGGTGGATCACG
AGGTCAGGAGTTTGTAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCTACAAAAATAC
AAAAATTAGCCGGGCCTGGTGGCGCTAATCCCAGTTACTCGGGAGGCTGAGGCAGGAGAA
TCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATCGCACCACTGCACTCCAGC
CTGGGCGACAGAGCAAGATTCTGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAGATGAA



FIGURE 3D



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Inventors: KETCHUM, Karen A. et al.
Title: ISOLATED HUMAN TRANSPORTER...

3064

CGGGGTGGATCACGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGTGAAACCCCGT
CTCTACAAAAATACAAAAATTAGCCGGGCTGGTGGCGCTAATCCAGTTACTCGGGAGG
CTGAGGCAGGAGATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATCGCAC
CACTGCACTCCAGCCTGGGCGACAGAGCAAGATTCTGTCTCAAAAAAAAAAAAAAAAAA
AAAAAAAAAGATGAAACCAAGTATACAAGCCCAGAAGCCTAGGGCTAATGGGACTGGAGTG
[C, T]

AAAAGGAAGAATTACTATAAAATGGTGCTAGGGGCCAGGCACGGTGGCTCACGCCTGTAA
TCCCAGCACTTTGGGAGGCGGAGGCGGATCACGAGGTCAGGAGATCAAGACCATCC
TGGCTAACACGGTGAAATCACGTCTCTACTAAAAACACAAAAAATTAGCTGGGCGTGCTG
GCAGGTGACTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATGGTGTAACCCGG
GAAGCAGAGCTTGAGTGAGCCGAGATTGCACCACTGCACTCCAGCCTGGGCGACAGAGC

4146

GTCCTGTTATTTCTCTCGCCGACGATCCCTGGCCACCGGGCTGGCACTGACAGGCGTGGG
CCTCTCCTCCTTACATTTGCCCCCTTTTCCAGTGGCTGCTCAGCCACTACGCCTGGAG
GGGGTCCCTGCTGCTGGTGTCTGCCCTCTCCCTCCACCTAGTGGCCTGTGGTGTCTCCT
CCGCCCCCTCCCTGGCTGAGGACCTGCTGTGGGTGGTCCCAGGGCCCACTCACCTC
TCTCCTCCATCATGGCCCCCTTCTCCGTTACACTGTTGCCCTCACCTGATCAACACTGG
[C, A]

TACTTCATTCCCTACCTCCACCTGGTGGCCCATCTCCAGGACCTGGATTGGGACCCACTA
CCTGCTGCCTTCTACTCTCAGTTGTTGCTATTTCTGACCTCGTGGGGCGTGTGGTCTCC
GGATGGCTGGGAGATGCAGTCCCAGGGCCTGTGACACGACTCCTGATGCTCTGGACCACC
TTGACTGGGGTGTCACTAGCCCTGTTCCCTGTAGCTCAGGCTCCCACAGCCCTGGTGGCT
CTGGCTGTGGCTACGGCTTACATCAGGGGCTCTGGCCCCACTGGCCTTCTCTGTGCTG

4440

CACTGGCTACTTCATTCCCTACCTCCACCTGGTGGCCCATCTCCAGGACCTGGATTGGGA
CCCACTACCTGCTGCCTTCTACTCTCAGTTGTTGCTATTTCTGACCTCGTGGGGCGTGT
GGTCTCCGGATGGCTGGGAGATGCAGTCCCAGGGCCTGTGACACGACTCCTGATGCTCTG
GACCACCTTGACTGGGGTGTCACTAGCCCTGTTCCCTGTAGCTCAGGCTCCCACAGCCCT
GGTGGCTCTGGCTGTGGCTACGGCTTACATCAGGGGCTCTGGCCCCACTGGCCTTCTC
[T, C]

GTGCTGCCTGAACATAATAGGGACTAGAAGGATTTACTGTGGCCTGGGACTGTTGCAGATG
ATAGAGAGCATCGGGGGGCTGCTGGGGCCTCCTCTCTCAGGTAAGTGAATGGGGTTCCC
AGGGGGTGAGGGCTGCCATGTTGCACAACTAGGGGAGGGTACTATTCTCATTACAGTGTA
TGTGAATATTGCCCTCTGGTGTAGTACAGTACACAGCCTGCGTGGCCAACCATAGCATCC
CTGAAATGGGTCCATGGGGCAAAGAACTTGGGGCTGGGAAAGTCTGAGTGGAAGACAAAA

4443

TGGCTACTTCATTCCCTACCTCCACCTGGTGGCCCATCTCCAGGACCTGGATTGGGACCC
ACTACCTGCTGCCTTCTACTCTCAGTTGTTGCTATTTCTGACCTCGTGGGGCGTGTGGT
CTCCGGATGGCTGGGAGATGCAGTCCCAGGGCCTGTGACACGACTCCTGATGCTCTGGAC
CACCTTGACTGGGGTGTCACTAGCCCTGTTCCCTGTAGCTCAGGCTCCCACAGCCCTGGT
GGCTCTGGCTGTGGCTACGGCTTACATCAGGGGCTCTGGCCCCACTGGCCTTCTCTGT
[G, T]

CTGCCCTGAACATAATAGGGACTAGAAGGATTTACTGTGGCCTGGGACTGTTGCAGATGATA
GAGAGCATCGGGGGGCTGCTGGGGCCTCCTCTCTCAGGTAAGTGAATGGGGTTCCCAGG
GGGTGAGGGCTGCCATGTTGCACAACTAGGGGAGGGTACTATTCTCATTACAGTGATGT
GAATATTGCCCTCTGGTGTAGTACAGTACACAGCCTGCGTGGCCAACCATAGCATCCCTG
AAATGGGTCCATGGGGCAAAGAACTTGGGGCTGGGAAAGTCTGAGTGGAAGACAAAAAG

5105

CCTGGCCAGACACAGACGTAGCATTCAGTGTGCACCCTTTCCTTTGGCCTACTGGGCCC
CAAACCAGGTATCTGAGGCACCTGGTCAAAGTTCTGCTGGCTCAGGGTGCCAGAACTTTC
AGACCTTTATCTCCTCTTACCCATTAAGCTTTAGAAAAGGCCACAGTTGGTGGGGCG
CCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATGGCATGAACCCGGGAGGCGG
AGCTTGCACTGAGCTGAGATCGCGCCACTGCACTTCAGCCTGGGCGACAGAGCGAGACTC
[T, C]

GTCTCAAAAAAAAAAAAAAAAAAGAAAGGCCACAGTTGCCAGAAAGAAAGGCACAAGTATGC
CTGACTCAATCTGGATCTCCAATCCCTGCAGGCTGGTTTGGAGGTCTTTCTGAAGGCG
GGGAGGTGGTTGAAATTAACTTTGGAGGCCCTTTGGGAAACCAGAGTTCTTAAGTTTAT
CCAATATTCCATGGGAGTTCCAATCCTCTGAGATGATAAGTCTTCCCTCCACCCAAAA
ATGTATCTGAGCCCTCAGCCCCAGCAAATAGATCACTCATGTGTATTCTTTTCTCTCTT

FIGURE 3E